

Breast Cancer Classifier from Image Analysis of Cell Nuclei Data using XGBoost Model

The following notebook demonstrates a complete machine learning workflow using the Breast Cancer Wisconsin dataset. The steps include data exploration, preprocessing, training an XGBoost classifier, and evaluating the model's performance.

Objective:

- Fetch/inspect dataset
- No missing values in this dataset, encode categorical target variable to numerical
- Train an XGBoost model
- Evaluate model performance and feature importance:
 - Feature importance plot
 - Masked correlation matrix
 - Confusion Matrix
- Explore correlation matrix for any continued investigation or dimension reduction
- Discussion, Conclusions, Potential Next Steps

```
In [10]: # Import necessary Libraries
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from xgboost import XGBClassifier
from sklearn.metrics import accuracy_score, classification_report, confusion_matrix
import warnings
warnings.filterwarnings('ignore', category=FutureWarning)
```

Fetch and Inspect the Data

Download dataset from the UCI Machine Learning Repository via <https://archive.ics.uci.edu/dataset/17/breast+cancer+wisconsin+diagnostic> become familiar with the structure and inspect data for missing values.

```
In [2]: # fetch dataset
data = pd.read_csv('C:\\Users\\alexm\\Desktop\\Data\\breast_cancer_data.csv')

# Display the first 5 rows
print("Display first 5 rows: \n", data.head(5))
```

```
# Display summary stats
print("Display Summary Statistics: \n", data.describe())

# Display basic info
print("==>Display basic information about the dataset:\n", data.info())

#Check for missing values
print("missing values:\n",data.isnull().sum())
```

Display first 5 rows:

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	842302	M	17.99	10.38	122.80	1001.0	
1	842517	M	20.57	17.77	132.90	1326.0	
2	84300903	M	19.69	21.25	130.00	1203.0	
3	84348301	M	11.42	20.38	77.58	386.1	
4	84358402	M	20.29	14.34	135.10	1297.0	

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	\
0	0.11840	0.27760	0.3001	0.14710	
1	0.08474	0.07864	0.0869	0.07017	
2	0.10960	0.15990	0.1974	0.12790	
3	0.14250	0.28390	0.2414	0.10520	
4	0.10030	0.13280	0.1980	0.10430	

	...	texture_worst	perimeter_worst	area_worst	smoothness_worst	\
0	...	17.33	184.60	2019.0	0.1622	
1	...	23.41	158.80	1956.0	0.1238	
2	...	25.53	152.50	1709.0	0.1444	
3	...	26.50	98.87	567.7	0.2098	
4	...	16.67	152.20	1575.0	0.1374	

	compactness_worst	concavity_worst	concave points_worst	symmetry_worst	\
0	0.6656	0.7119	0.2654	0.4601	
1	0.1866	0.2416	0.1860	0.2750	
2	0.4245	0.4504	0.2430	0.3613	
3	0.8663	0.6869	0.2575	0.6638	
4	0.2050	0.4000	0.1625	0.2364	

	fractal_dimension_worst	Unnamed: 32
0	0.11890	NaN
1	0.08902	NaN
2	0.08758	NaN
3	0.17300	NaN
4	0.07678	NaN

[5 rows x 33 columns]

Display Summary Statistics:

	id	radius_mean	texture_mean	perimeter_mean	area_mean	\
count	5.690000e+02	569.000000	569.000000	569.000000	569.000000	
mean	3.037183e+07	14.127292	19.289649	91.969033	654.889104	
std	1.250206e+08	3.524049	4.301036	24.298981	351.914129	
min	8.670000e+03	6.981000	9.710000	43.790000	143.500000	
25%	8.692180e+05	11.700000	16.170000	75.170000	420.300000	
50%	9.060240e+05	13.370000	18.840000	86.240000	551.100000	
75%	8.813129e+06	15.780000	21.800000	104.100000	782.700000	
max	9.113205e+08	28.110000	39.280000	188.500000	2501.000000	

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	\
count	569.000000	569.000000	569.000000	569.000000	
mean	0.096360	0.104341	0.088799	0.048919	
std	0.014064	0.052813	0.079720	0.038803	
min	0.052630	0.019380	0.000000	0.000000	
25%	0.086370	0.064920	0.029560	0.020310	
50%	0.095870	0.092630	0.061540	0.033500	
75%	0.105300	0.130400	0.130700	0.074000	

max	0.163400	0.345400	0.426800	0.201200
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	symmetry_mean	...	texture_worst	perimeter_worst	area_worst	\
count	569.000000	...	569.000000	569.000000	569.000000	
mean	0.181162	...	25.677223	107.261213	880.583128	
std	0.027414	...	6.146258	33.602542	569.356993	
min	0.106000	...	12.020000	50.410000	185.200000	
25%	0.161900	...	21.080000	84.110000	515.300000	
50%	0.179200	...	25.410000	97.660000	686.500000	
75%	0.195700	...	29.720000	125.400000	1084.000000	
max	0.304000	...	49.540000	251.200000	4254.000000	

	smoothness_worst	compactness_worst	concavity_worst	\
count	569.000000	569.000000	569.000000	
mean	0.132369	0.254265	0.272188	
std	0.022832	0.157336	0.208624	
min	0.071170	0.027290	0.000000	
25%	0.116600	0.147200	0.114500	
50%	0.131300	0.211900	0.226700	
75%	0.146000	0.339100	0.382900	
max	0.222600	1.058000	1.252000	

	concave points_worst	symmetry_worst	fractal_dimension_worst	\
count	569.000000	569.000000	569.000000	
mean	0.114606	0.290076	0.083946	
std	0.065732	0.061867	0.018061	
min	0.000000	0.156500	0.055040	
25%	0.064930	0.250400	0.071460	
50%	0.099930	0.282200	0.080040	
75%	0.161400	0.317900	0.092080	
max	0.291000	0.663800	0.207500	

Unnamed: 32

count	0.0
mean	NaN
std	NaN
min	NaN
25%	NaN
50%	NaN
75%	NaN
max	NaN

[8 rows x 32 columns]

<class 'pandas.core.frame.DataFrame'>

RangeIndex: 569 entries, 0 to 568

Data columns (total 33 columns):

#	Column	Non-Null Count	Dtype
---	-----	-----	-----
0	id	569 non-null	int64
1	diagnosis	569 non-null	object
2	radius_mean	569 non-null	float64
3	texture_mean	569 non-null	float64
4	perimeter_mean	569 non-null	float64
5	area_mean	569 non-null	float64
6	smoothness_mean	569 non-null	float64
7	compactness_mean	569 non-null	float64

8	concavity_mean	569 non-null	float64
9	concave points_mean	569 non-null	float64
10	symmetry_mean	569 non-null	float64
11	fractal_dimension_mean	569 non-null	float64
12	radius_se	569 non-null	float64
13	texture_se	569 non-null	float64
14	perimeter_se	569 non-null	float64
15	area_se	569 non-null	float64
16	smoothness_se	569 non-null	float64
17	compactness_se	569 non-null	float64
18	concavity_se	569 non-null	float64
19	concave points_se	569 non-null	float64
20	symmetry_se	569 non-null	float64
21	fractal_dimension_se	569 non-null	float64
22	radius_worst	569 non-null	float64
23	texture_worst	569 non-null	float64
24	perimeter_worst	569 non-null	float64
25	area_worst	569 non-null	float64
26	smoothness_worst	569 non-null	float64
27	compactness_worst	569 non-null	float64
28	concavity_worst	569 non-null	float64
29	concave points_worst	569 non-null	float64
30	symmetry_worst	569 non-null	float64
31	fractal_dimension_worst	569 non-null	float64
32	Unnamed: 32	0 non-null	float64

dtypes: float64(31), int64(1), object(1)

memory usage: 146.8+ KB

==>Display basic information about the dataset:

None

missing values:

id	0
diagnosis	0
radius_mean	0
texture_mean	0
perimeter_mean	0
area_mean	0
smoothness_mean	0
compactness_mean	0
concavity_mean	0
concave points_mean	0
symmetry_mean	0
fractal_dimension_mean	0
radius_se	0
texture_se	0
perimeter_se	0
area_se	0
smoothness_se	0
compactness_se	0
concavity_se	0
concave points_se	0
symmetry_se	0
fractal_dimension_se	0
radius_worst	0
texture_worst	0
perimeter_worst	0
area_worst	0

```
smoothness_worst      0
compactness_worst     0
concavity_worst       0
concave points_worst  0
symmetry_worst        0
fractal_dimension_worst 0
Unnamed: 32           569
dtype: int64
```

Data Preprocessing

1. Drop unneeded column for a more efficient model
2. Create Feature and Target variables
3. Convert categorical target variable (M = malignant, B = benign) to binary

```
In [3]: # Drop the ID column
data = data.drop(['Unnamed: 32', 'id'], axis=1)

# Create Features and Target Variable
X = data.drop('diagnosis', axis=1)
y = data['diagnosis']

#convert Target variable to binary
y = y.replace({'M':1, 'B':0})
```

Data Splitting, Scaling, and XGboost Training

Splitting the data is necessary for training and evaluating the performance of the model. Normalizing the features with StandardScaler() can enhance the performance and convergence speed of XGboost algorithm.

stratify=y in the train_test_split function is important for maintaining the same proportion of classes in both the training and testing sets as in the original dataset. Here's a detailed explanation:

```
In [16]: # split the dataset for training and test sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, stratify=y)

# Standardize the variables
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)

#Initialize the XGBoost Classifier
model = XGBClassifier()

# Train the model
```

```

model.fit(X_train, y_train)

# make predictions
y_pred = model.predict(X_test)

# Evaluate the model
accuracy = accuracy_score(y_test, y_pred)
print(f"Accuracy: {accuracy:.2f}")

# Print classification report
print("Classification Report:\n", classification_report(y_test, y_pred))

```

Accuracy: 0.98

Classification Report:

	precision	recall	f1-score	support
0	0.96	1.00	0.98	107
1	1.00	0.94	0.97	64
accuracy			0.98	171
macro avg	0.98	0.97	0.97	171
weighted avg	0.98	0.98	0.98	171

Data Visualization

Visualization enables us to explore the data in a more digestible way and evaluate the performance in a more intuitively.

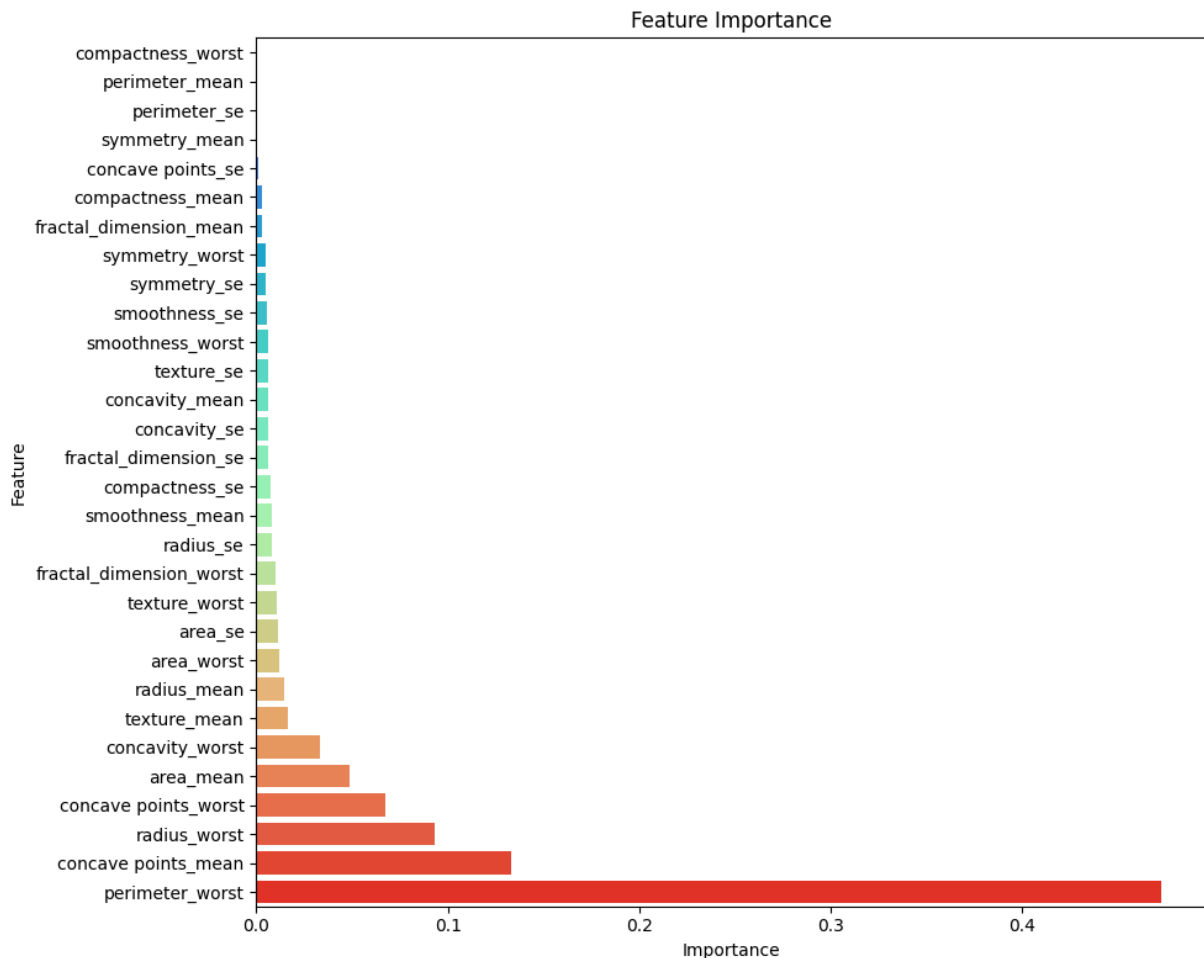
1. Plot Feature Importance

Understand what features contribute most to the models performance.

```

In [17]: # Get feature importance
importance = model.feature_importances_
# Convert into a pandas DataFrame
features = pd.DataFrame({'Feature': X.columns, 'Importance': importance})
# Sort the features by importance
features = features.sort_values(by='Importance', ascending=True)
# Plot feature importance
plt.figure(figsize=(10, 8))
sns.barplot(x='Importance', y='Feature', data=features, palette='rainbow')
plt.title('Feature Importance')
plt.tight_layout()
plt.show()

```



2. Correlation Matrix Observe the relationship of the feature vs. the target. Understand redundancy can be cleaned up for further model efficiency. A mask was applied for more intuitive viewing by eliminating redundancy.

```
In [18]: # Convert Target categorical variable to numerical binary
data['diagnosis'] = data['diagnosis'].replace({'M': 1, 'B': 0})

# Calculate the correlation matrix
corr = data.corr()

# Generate a mask for the upper triangle
mask = np.triu(np.ones_like(corr, dtype=bool))

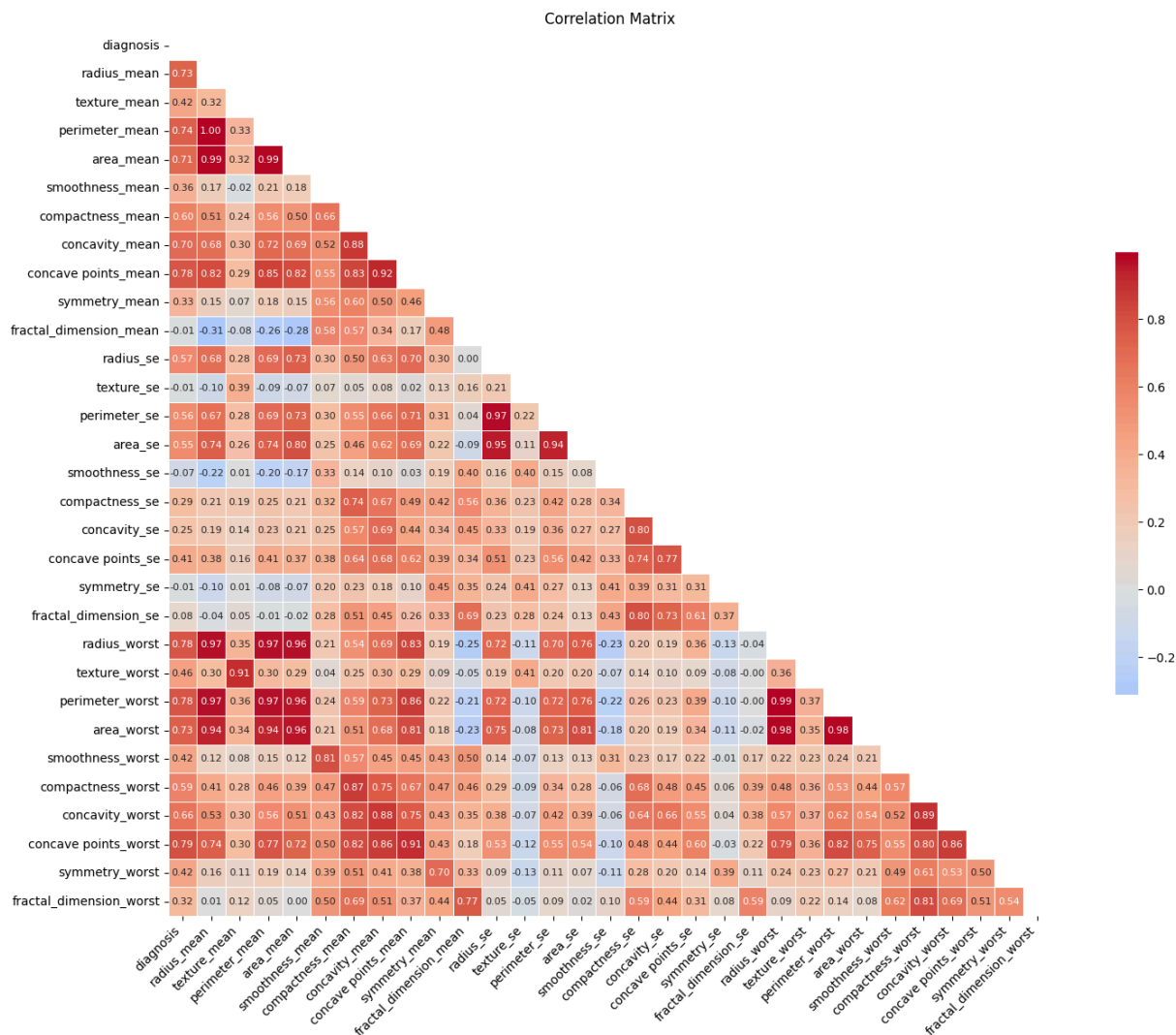
# Set up the matplotlib figure
plt.figure(figsize=(16, 12))

# Draw the heatmap with the mask and correct aspect ratio
sns.heatmap(corr, mask=mask, cmap='coolwarm', center=0, annot=True, fmt=".2f",
            square=True, linewidths=0.5, cbar_kws={"shrink": 0.5}, annot_kws={"size": 10})

plt.title('Correlation Matrix')
plt.xticks(rotation=45, ha='right', fontsize=10)
plt.yticks(fontsize=10)
```



```
plt.tight_layout()
plt.show()
```



3. Confusion Matrix

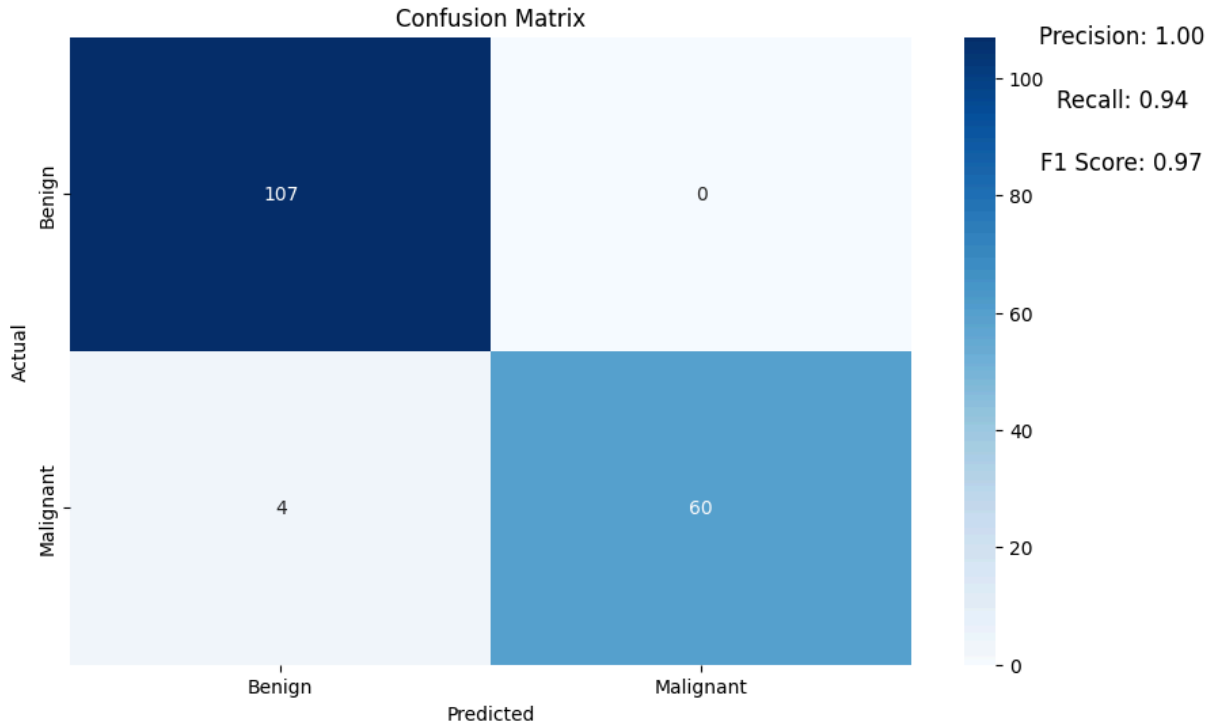
Shows the number of true positives, true negatives, false positives, and false negatives.

```
In [20]: # Compute confusion matrix
cm = confusion_matrix(y_test, y_pred)

# Compute precision, recall, and F1 score
precision, recall, f1, _ = precision_recall_fscore_support(y_test, y_pred, average='macro')

# Plot confusion matrix with additional metrics
plt.figure(figsize=(10, 6))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues',
            xticklabels=['Benign', 'Malignant'],
            yticklabels=['Benign', 'Malignant'])
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix')
# Adding the precision, recall, and F1 score text to the plot
```

```
plt.text(2.5, 0, f'Precision: {precision:.2f}', ha='center', va='center', fontsize=12)
plt.text(2.5, .2, f'Recall: {recall:.2f}', ha='center', va='center', fontsize=12)
plt.text(2.5, .4, f'F1 Score: {f1:.2f}', ha='center', va='center', fontsize=12)
plt.show()
```



1.0 0.9375 0.967741935483871

Conclusions

1. Model Performance: The XGBoost model used in the analysis demonstrated a high accuracy score of 98%, high precision (1.0) and very good recall (0.9375), resulting in an F1 score of approximately 0.9677. This indicates that the model is highly effective at identifying malignant cases without producing many false positives. High accuracy in the model suggests that it is reliable for predicting breast cancer diagnosis, with a low probability of misclassification.
2. Feature Importance: The feature importance plot highlighted perimeter_worst,concave points_mean, radius_worst were most influential in predicting the diagnosis. This information can be used to focus on the most critical factors in future studies or to reduce model complexity with dimensional reduction. Furthermore, if we were to look upstream to optimize the image recognition software to target the predictor feature more intensely this could benefit the workflow accuracy.
3. Correlation Analysis: The correlation matrix showed how features are related to one another. Highly correlated features can be redundant and may lead to inefficiencies in the model, tree-based models like XGBoost are generally robust to these issues.

Discussion

1. Ethical Considerations: Using machine learning models for medical diagnoses requires careful consideration of ethical implications. False negatives, where the model fails to identify a malignant case (2% observed herer), could lead to serious consequences. Therefore, the model must be thoroughly tested and of course augmented with human oversight.
2. Generalization: The model's generalization to different populations or data sources needs to be carefully evaluated. Differences in demographics, medical practices, or data collection methods can affect the model's performance.
3. Collaboration with Medical Experts: Collaboration with healthcare professionals is crucial to ensure the model's predictions align with clinical insights and that the model is integrated into the diagnostic workflow appropriately.

Next Steps

1. Model Optimization:
 - Hyperparameter Tuning: Hyperparameter tuning was not explored yet for this dataset. The XGboost model could be optimized.
2. Feature Engineering:
 - Feature Selection: Perform additional feature selection or dimensionality reduction techniques (e.g., PCA) to simplify the model and possibly improve its performance should be considered if the model was to be scaled.
 - Interaction Features: Investigate creating interaction features, which might capture more complex relationships between features and the target variable or highlight areas for more study/optimization.
3. Deployment:
 - Real-world Testing: If there is desire for the model deployed in a clinical setting, it should be tested with more real-world data to ensure it performs as expected outside of the controlled environment set that was observed here.
 - Model Monitoring: Set up a monitoring system to track the model's performance over time, ensuring that it continues to perform well as new data becomes available.